



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Friedman, Jeffrey M.  
Lee, Gwo-Hua  
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC  
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 56

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.  
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
(C) CITY: Hackensack  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/586,594  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 600-1-162

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800  
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2529 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

RECEIVED  
NOV 27 2002  
TECH CENTER 1600/2900

GGGCTCAGGT	CGGCGTCGTA	CCAGCCGCTG	AAGCGGTTCT	CCAGGTTCCA	GGCGCTCTCG	60
CCATGCCGGA	TCAGCACCAG	CTTGTAGCTC	GTGCCGAATT	CGGCACGAGG	TTGCTTTGGG	120
AATGAGCAAG	GTCAAAACTG	CTCTGCACTC	ACAGACAACA	CTGAAGGGAA	GAACTGGCT	180
TCAGTAGTGA	AGGCTTCAGT	TTTTCGCCAG	CTAGGTGTAA	ACTGGGACAT	AGAGTGCTGG	240
ATGAAAGGGG	ACTTGACATT	ATTCATCTCT	CATATGGAGC	CATTACCTAA	GAACCCCTTC	300
AAGAATTATG	ACTCTAAGGT	CCATCTTTTA	TATGATCTGC	CTGAAGTCAT	AGATGATTCG	360
CCTCTGCCCC	CACTGAAAGA	CAGCTTTCAG	ACTGTCCAAT	GCAACTGCAG	TCTTCGGGGA	420
TGTGAATGTC	ATGTGCCGGT	ACCCAGAGCC	AAACTCAACT	ACGCTCTTCT	GATGTATTTG	480
GAAATCACAT	CTGCCGGTGT	GAGTTTTTCA	TCACCTCTGA	TGTCAGTGCA	GCCCATGCTT	540
GTTGTGAAAC	CCGATCCACC	CTTAGGTTTG	CATATGGAAG	TCACAGATGA	TGGTAATTTA	600
AAGATTTCTT	GGGACAGCCA	AACAATGGCA	CCATTTCCGC	TTCAATATCA	GGTGAAATAT	660
TTAGAGAATT	CTACAATTGT	AAGAGAGGCT	GCTGAAATTG	TCTCAGCTAC	ATCTCTGCTG	720
GTAGACAGTG	TGCTTCCTGG	ATCTTCATAT	GAGGTCCAGG	TGAGGAGCAA	GAGACTGGAT	780
GGTTCAGGAG	TCTGGAGTGA	CTGGAGTTCA	CCTCAAGTCT	TTACCACACA	AGATGTTGTG	840
TATTTTCCAC	CCAAAATTCT	GACTAGTGTT	GGATCGAATG	CTTCTTTTCA	TTGCATCTAC	900
AAAAACGAAA	ACCAGATTAT	CTCCTCAAAA	CAGATAGTTT	GGTGAGGAA	TCTAGCTGAG	960
AAAAATCCCTG	AGATACAGTA	CAGCATTGTG	AGTGACCGAG	TTAGCAAAGT	TACCTTCTCC	1020
AACCTGAAAG	CCACCAGACC	TCGAGGGAAG	TTTACCTATG	ACGCAGTGTA	CTGCTGCAAT	1080
GAGCAGGCGT	GCCATCACCG	CTATGCTGAA	TTATACGTGA	TCGATGTCAA	TATCAATATA	1140
TCATGTGAAA	CTGACGGGTA	CTTAACTAAA	ATGACTTGCA	GATGGTCACC	CAGCACAATC	1200
CAATCACTAG	TGGGAAGCAC	TGTGCAGCTG	AGGTATCACA	GGCGCAGCCT	GTATTGTCCCT	1260
GATAGTCCAT	CTATTCATCC	TACGTCTGAG	CCCAAAACT	GCGTCTTACA	GAGAGACGGC	1320
TTTTATGAAT	GTGTTTTCCA	GCCAATCTTT	CTATTATCTG	GCTATACAAT	GTGGATCAGG	1380
ATCAACCATT	CTTTAGGTTT	ACTTGACTCG	CCACCAACGT	GTGTCCTTCC	TGACTCCGTA	1440
GTAAAACCAC	TACCTCCATC	TAACGTAAAA	GCAGAGATTA	CTGTAAACAC	TGGATTATTG	1500
AAAGTATCTT	GGGAAAAGCC	AGTCTTTCCG	GAGAATAACC	TTCAATTCCA	GATTCGATAT	1560
GGCTTAAGTG	GAAAAGAAAT	ACAATGGAAG	ACACATGAGG	TATTCGATGC	AAAGTCAAAG	1620
TCTGCCAGCC	TGCTGGTGTC	AGACCTCTGT	GCAGTCTATG	TGGTCCAGGT	TCGCTGCCGG	1680
CGGTTGGATG	GACTAGGATA	TTGGAGTAAT	TGGAGCAGTC	CAGCCTATAC	GCTTGTCATG	1740
GATGTAAAAG	TTCTATGAG	AGGGCCTGAA	TTTTGGAGAA	AAATGGATGG	GGACGTTACT	1800
AAAAAGGAGA	GAAATGTCAC	CTTGCTTTGG	AAGCCCTTGA	CGAAAAATGA	CTCACTGTGT	1860
AGTGTGAGGA	GGTACGTGGT	GAAGCATCGT	ACTGCCCACA	ATGGGACGTG	GTCAGAAGAT	1920

GTGGGAAATC GGACCAATCT CACTTTCTCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT 1980  
 CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC 2040  
 ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC 2100  
 ATCCTTTCTT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG 2160  
 AAGATCCTTA ATGAAGATGA TGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG 2220  
 TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA 2280  
 TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC 2340  
 AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTT CTCTTGTCGTC 2400  
 CTACTGCTCG GAACACTGTT AATTTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT 2460  
 GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520  
 ACTCTTTGA 2529

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 842 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly	Leu	Arg	Ser	Ala	Ser	Tyr	Gln	Pro	Leu	Lys	Arg	Phe	Ser	Arg	Phe
1				5				10					15		
Gln	Ala	Leu	Ser	Pro	Cys	Arg	Ile	Ser	Thr	Ser	Leu	Xaa	Leu	Val	Pro
			20					25					30		
Asn	Ser	Ala	Arg	Gly	Cys	Phe	Gly	Asn	Glu	Gln	Gly	Gln	Asn	Cys	Ser
		35					40					45			
Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	Ser	Val	Val	Lys
		50				55				60					
Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	Ile	Glu	Cys	Trp
65				70					75					80	
Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	Glu	Pro	Leu	Pro
			85					90					95		
Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	Leu	Leu	Tyr	Asp

100										105					110				
Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	Leu	Lys	Asp	Ser				
		115					120					125							
Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	Cys	Glu	Cys	His				
	130					135					140								
Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu				
145					150					155					160				
Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu				
				165					170					175					
Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met				
			180					185					190						
Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr				
		195					200					205							
Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser				
	210					215					220								
Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu				
225					230					235					240				
Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser				
				245					250					255					
Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln				
			260					265					270						
Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr				
		275					280					285							
Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn				
	290					295					300								
Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu				
305					310				315						320				
Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	Arg	Val	Ser	Lys				
				325					330					335					
Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	Gly	Lys	Phe	Thr				
			340					345					350						
Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	His	His	Arg	Tyr				
	355						360					365							
Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	Ser	Cys	Glu	Thr				
	370					375					380								
Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Pro	Ser	Thr	Ile				
385					390					395					400				
Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr	His	Arg	Arg	Ser				
				405					410				415						
Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr	Ser	Glu	Pro	Lys				
			420					425					430						
Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys	Val	Phe	Gln	Pro				
		435					440					445							

Sub C37

Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg	Ile	Asn	His	Ser		
450						455					460						
Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu	Pro	Asp	Ser	Val		
465					470					475					480		
Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu	Ile	Thr	Val	Asn		
				485					490					495			
Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val	Phe	Pro	Glu	Asn		
			500					505					510				
Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly	Lys	Glu	Ile	Gln		
		515					520					525					
Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys	Ser	Ala	Ser	Leu		
	530					535						540					
Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln	Val	Arg	Cys	Arg		
545					550					555					560		
Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser	Ser	Pro	Ala	Tyr		
				565					570					575			
Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly	Pro	Glu	Phe	Trp		
			580					585					590				
Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg	Asn	Val	Thr	Leu		
		595					600					605					
Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg		
	610					615					620						
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp		
625					630					635					640		
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His		
				645					650					655			
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn		
			660					665					670				
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu		
		675					680					685					
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp		
	690					695					700						
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp		
705					710					715					720		
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser		
				725					730					735			
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys		
			740					745					750				
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro		
	755						760					765					
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn		
	770					775					780						

Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val  
 785 790 795 800  
 Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu  
 805 810 815  
 Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly  
 820 825 830  
 Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu  
 835 840

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2848 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT	60
GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG	120
GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATTT TAGAATGGGA AGAATTAGGA	180
AGATGAATGG AGCCTGTGTC TTCTACTACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG	240
TCAGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAG	300
CCTGGGTTAC TTCTTATCAT CCTTAATTTT GAAAGCTAAG AGGGCCTAAC CATCAAGAAC	360
GTCCTGGAGG AAAGAATGTT TTTAACGCCA TTATTCAGTC AAAGAAATTA AGACTTGAGA	420
GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA	480
TGNGGCCCTA CCCACGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTTCTAACTC	540
AGAGACTCTT GTTCTAGTCT GTGNTATAAA ATTCAGCTTG TGGAGCTTT CTGAGGGGTT	600
GGCAGCATTC AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGTT	660
ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC	720
TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCCC AGGGCCCCAA	780
AATAGCCGCT GTTATTTGTT AACCTTCAAG GTTTTCTGTT TGTTTATCTG TTTCTTGCGC	840
AGGATCATCT TCCAAGCACA TCCTGGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA	900

CTATGGTGAC	ATCTGAGCTT	CCTTGGTTCT	TCACAGAACA	TAAGCAGTTC	CTTTGCTTGC	960
TTGTTAGATG	AGAAAACCTC	CTTGTCAGTC	TGTCTCTACG	ACTAGAATGG	AAAGCCTTAC	1020
TACTTCCTAT	GTATTCTTAA	TATTTCAAAT	GTCCTAATTA	TGTTTGGCTT	CTCTGTCTTT	1080
AAGGGATTTA	GTCTCTGGAT	TTGAAGAAAT	AAATAAATAA	ATAAAGGAAA	ACTAATTTTC	1140
TCGTGCCGGA	TGACTGCTAG	CTGAGCTCAG	GCCTACTGCA	TTCTACATTT	CGACTCTCTC	1200
CCTCTTCCCC	AGTGCTTTAG	CACTGGACTG	GGCAGTNCCT	GGCCTGGTCT	AACTCCTGTT	1260
TCCTGGTGGG	AATGTATAAT	AAGAACTCCA	TCAGTTCTGG	TATAAACACT	GTGGTCTGTG	1320
TGCTAATTAA	ATCTNGTGTT	TCCTACAGCC	CCTGACGAAA	AATGACTCAC	TGTGTAGTGT	1380
GAGGAGGTAC	GTGGTGAAGC	ATCGTACTGC	CCACAATGGG	ACGTGGTCAG	AAGATGTGGG	1440
AAATCGGACC	AATCTCACTT	TCCTGTGGAC	AGAACCAGCG	CACACTGTTA	CAGTTCTGGC	1500
TGTCAATTCC	CTCGGCGCTT	CCCTTGTGAA	TTTTAACCTT	ACCTTCTCAT	GGCCCATGAG	1560
TAAAGTGAGT	GCTGTGGAGT	CACTCAGTGC	TTATCCCCTG	AGCAGCAGCT	GTGTCATCCT	1620
TTCTTGGA	CTGTACCTG	ATGATTATAG	TCTGTTATAT	CTGGTTATTG	AATGGAAGAT	1680
CCTTAATGAA	GATGATGGAA	TGAAGTGGCT	TAGAATFCCC	TCGAATGTTA	AAAAGTTTTA	1740
TATCCACGAT	AATTTTATTC	CCATCGAGAA	ATATCAGTTT	AGTCTTTACC	CAGTATTTAT	1800
GGAAGGAGTT	GGAAAACCAA	AGATAATTAA	TGGTTTCACC	AAAGATGCTA	TCGACAAGCA	1860
GCAGAATGAC	GCAGGGCTGT	ATGTCATTGT	ACCCATAATT	ATTTCTCTTT	GTGTCCTACT	1920
GCTCGGAACA	CTGTTAATTT	CACACCAGAG	AATGAAAAAG	TTGTTTTGGG	ACGATGTTCC	1980
AAACCCCAAG	AATTGTTTCT	GGGCACAAGG	ACTGAATTTT	CAAAAGCCTG	AAACATTNGA	2040
GCATCTTTTT	ACCAAGCATG	CAGAATCAGT	GATATTTGGT	CCTCTTCTTC	TGGAGCCTGA	2100
ACCCATTTCA	GAAGAAATCA	GTGTCGATAC	AGCTTGGAAG	AATAAAGATG	AGATGGTCCC	2160
AGCAGCTATG	GTCTCCCTNC	TNNGGACCAC	ACCAGACCTT	GAAAGCAGTT	CTATTTGTNT	2220
TAGTGACCAG	TGTAACAGTG	CTAACTTCTC	TGGGTCTCAG	AGCACCCAGG	TAACCTGTGA	2280
GGATGAGTGT	CAGAGACAAC	CCTCAGTTAA	ATATGCAACT	CTGGTCAGCA	ACGATAAACT	2340
AGTGGAAGT	GATGAAGAGC	AAGGGTTTAT	CCATAGTCCT	GTCAGCAACT	GCATCTCCAG	2400
TAATCATTTT	CCACTGAGGC	AGTCTTTCTC	TAGCAGCTCC	TGGGAGACAG	AGGCCCAGAC	2460
ATTTTTCTCT	TTATCAGACC	AGCAACCCAC	CATGATTTCA	CCACAACCTT	CATTCTCGGG	2520
GTTGGATGAG	CTTTTGGAAC	TGGAGGGAAG	TTTTCTTGAA	GAAAATCACA	GGGAGNAGTC	2580
TGTCTGTTAT	CTAGGAGTCA	CCTCCGTCCN	CAGAAGAGAG	AGTGGTGTGC	TTTTGACTGG	2640
TGAGGCAGGA	ATCCTGTGCA	CATTCCCAGC	CCAGTGTCTG	TTCAGTGACA	TCAGGATCCT	2700
CCAGGAGAGA	TGCTCACACT	TTGTAGAAAA	TAATTTGAGT	TTAGGGACCT	CTGGTGAGAA	2760
CTTTGGTCCT	AACATGCCCC	AATTCCAAAC	CTGTTCCACG	CACAGTCACA	AGATAATGGA	2820

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 581 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Ile	Lys	Glu
1				5				10						15	
Asn	Phe	Ser	Arg	Ala	Gly	Leu	Leu	Ala	Glu	Leu	Arg	Pro	Thr	Ala	Phe
			20					25					30		
Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala	Leu	Asp	Trp
		35					40					45			
Ala	Val	Pro	Gly	Leu	Val	Leu	Leu	Phe	Pro	Gly	Gly	Asn	Val	Glu	Leu
	50					55					60				
His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu	Cys	Ala	Asn	Ile	Xaa	Cys
65					70					75					80
Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg
				85					90					95	
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp
			100					105						110	
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His
		115					120					125			
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn
		130				135					140				
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu
145					150					155					160
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp
				165					170					175	
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp
			180					185					190		
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser
		195					200						205		
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys

210					215					220					
Tyr 225	Gln	Phe	Ser	Leu	Tyr 230	Pro	Val	Phe	Met	Glu 235	Gly	Val	Gly	Lys	Pro 240
Lys	Ile	Ile	Asn	Gly 245	Phe	Thr	Lys	Asp	Ala 250	Ile	Asp	Lys	Gln	Gln	Asn 255
Asp	Ala	Gly	Leu	Tyr 260	Val	Ile	Val	Pro 265	Ile	Ile	Ile	Ser	Ser	Cys	Val 270
Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile 280	Ser	His	Gln	Arg	Met	Lys	Lys	Leu 285
Phe 290	Trp	Asp	Asp	Val	Pro	Asn 295	Pro	Lys	Asn	Cys	Ser 300	Trp	Ala	Gln	Gly
Leu 305	Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln 315	Leu	Phe	Thr	Lys	His 320
Ala	Glu	Ser	Val	Ile 325	Phe	Gly	Pro	Leu	Leu	Leu 330	Glu	Pro	Glu	Pro	Ile 335
Ser	Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala 345	Trp	Lys	Asn	Lys	Asp	Glu	Met 350
Val	Pro	Ala	Ala	Met	Val	Ser	Leu 360	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu 365
Ser 370	Ser	Ser	Ile	Cys	Ile	Ser	Asp 375	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser 380
Gly 385	Ser	Gln	Ser	Thr	Gln	Val	Cys 390	Glu	Asp	Glu 395	Cys	Gln	Arg	Gln	Pro 400
Ser	Val	Lys	Tyr	Ala 405	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr 415
Asp	Glu	Glu	Gln	Gly	Phe	Ile	His 425	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser 430
Ser	Asn	His	Ser	Pro	Leu	Arg	Gln 440	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu 445
Thr 450	Glu	Ala	Gln	Thr	Phe	Phe	Leu 455	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met 460
Ile 465	Ser	Pro	Gln	Leu	Ser	Phe	Ser 470	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu 480
Glu	Gly	Ser	Phe	Pro	Glu	Glu	Asn	His 490	Arg	Glu	Lys	Ser	Val	Cys	Tyr 495
Leu	Gly	Val	Thr	Ser	Val	Asn	Arg 505	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr 510
Gly	Glu	Ala	Gly	Ile	Leu	Cys	Thr 520	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser 525
Asp 530	Ile	Arg	Ile	Leu	Gln	Glu	Arg 535	Cys	Ser	His	Phe	Val	Glu	Asn	Asn 540
Leu 545	Ser	Leu	Gly	Thr	Ser	Gly	Glu 550	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln 560

Phe Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met  
565 570 575

Cys Asp Phe Thr Val  
580

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTTCCTGGT GGGAATGTAT AATAAGAACT COATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT	540
CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720
TATGGAAGGA GTTGGAAGAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTAACCATTA ATTATTTTCT CTTGTGTCCT	840
ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAAATGAAA AAGTTGTTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA	960
A	961

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 319 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
    (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Xaa	Ile	Lys
1				5				10						15	
Glu	Asn	Xaa	Phe	Ser	Arg	Ala	Gly	Xaa	Leu	Leu	Ala	Glu	Leu	Arg	Pro
			20					25						30	
Thr	Ala	Phe	Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala
			35				40						45		
Leu	Asp	Trp	Ala	Val	Pro	Gly	Leu	Val	Xaa	Leu	Leu	Phe	Pro	Gly	Gly
			50				55						60		
Asn	Val	Xaa	Xaa	Glu	Leu	His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu
65					70					75					80
Cys	Ala	Asn	Xaa	Ile	Xaa	Cys	Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp
				85					90						95
Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His
				100					105					110	
Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe
				115									125		
Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser
						135						140			
Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met
145					150					155					160
Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser
					165				170					175	
Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu
				180					185					190	
Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met
							200					205			
Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp
							215					220			
Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe

225		230		235		240
Met Glu Gly Val	Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp					
	245			250		255
Ala Ile Asp Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro						
	260			265		270
Ile Ile Ile Ser Ser Cys Val	Leu Leu Leu Gly Thr Leu Leu Ile Ser					
	275			280		285
His Gln Arg Met Lys Lys Leu	Phe Trp Asp Asp Val Pro Asn Pro Lys					
	290			295		300
Asn Cys Ser Trp Ala Gln Gly	Leu Asn Phe Gln Lys Val Thr Val					
	305			310		315

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2703 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTAACTGGG AATTTCTTTA TGTGATAGCT	60
GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGCAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTAAATT CAAGTGGTAT CTACGTTCTT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAAGTGTCTT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGCATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCCTC TGCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTG TGAAACCCGA TCCACCCTTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTTGGGA CAGCCAAACA	780

ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGA CTGG	960
AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTGATG	CGAATGCTTC	TTTTCATTCG	ATCTACAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAAGTGGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACCT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAAG	TATCTTGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTGAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	CTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCTT	GAGCAGCAGC	TCTGTCTATC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTTAC	CCAGTATTTA	TGGAAGGAGT	TGGAAAACCA	2460
AAGATAATTA	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520
TATGTCATTG	TACCCATAAT	TATTTCTCTT	TGTGTCTCTAC	TGCTCGGAAC	ACTGTTAATT	2580
TCACACCAGA	GAATGAAAAA	GTTGTTTTGG	GACGATGTTT	CAAACCCCAA	GAATTGTTCC	2640
TGGGCACAAG	GA CTGAATTT	CCAAAAGGAT	ATATCTTTAC	ATGAAGTTTT	TATTTTCAGA	2700

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 900 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:  
    (B) CLONE: OB-Rd

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1				5					10					15	
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys
			20					25					30		
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu
		35					40					45			
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser
	50					55					60				
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro
65				70					75						80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly
			85					90						95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala
		100						105					110		
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp
	115						120					125			
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met
	130					135					140				
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His
145				150					155					160	
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro
			165					170					175		
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly
		180						185					190		
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu
	195						200					205			

Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro
210						215					220				
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu
225					230					235					240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp
				245					250					255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr
			260					265					270		
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala
		275					280					285			
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
		290				295					300				
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp
305					310					315					320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro
				325					330					335	
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr
			340					345					350		
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg
		355					360					365			
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp
		370				375					380				
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg
385					390					395					400
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys
				405					410					415	
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile
			420					425					430		
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser
		435					440					445			
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr
		450				455					460				
His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
465					470					475					480
Ser	Glu	Pro	Lys	Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys
				485					490					495	
Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg
			500					505					510		
Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu
		515					520					525			
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu
		530				535					540				
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val

545		550		555		560									
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly
				565					570					575	
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys
			580					585					590		
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln
		595					600					605			
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser
	610					615					620				
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly
625					630					635					640
Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg
				645					650					655	
Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys
			660					665					670		
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr
		675					680					685			
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr
	690					695					700				
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala
705					710					715					720
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val
				725				730						735	
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val
			740					745					750		
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu
		755					760					765			
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu
	770					775					780				
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile
785					790					795					800
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly
				805					810					815	
Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp
			820					825					830		
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile
		835					840					845			
Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg
		850				855					860				
Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser
865					870					875					880
Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Asp	Ile	Ser	Leu	His	Glu	Val
				885					890					895	

Phe Ile Phe Arg  
900

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2461 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGAATCGT TCTGCAAATC CAGGTGTACA CCTCTGAAGA AAGATGATGT GTCAGAAATT	60
CTATGTGGTT TTGTTACACT GGAATTTCT TTATGTGATA GCTGCACTTA ACCTGGCATA	120
TCCAATCTCT CCCTGGAAAT TTAAGTTGTT TTGTGGACCA CCGAACACAA CCGATGACTC	180
CTTTCTCTCA CCTGCTGGAG CCCCAAACAA TGCTTCGGCT TTGAAGGGGG CTTCTGAAGC	240
AATTGTTGAA GCTAAATTTA ATTCAAGTGG TATCTACGTT CCTGAGTTAT CCAAAACAGT	300
CTTCCACTGT TGCTTTGGGA ATGAGCAAGG TCAAACTGC TCTGCACTCA CAGACAACAC	360
TGAAGGGAAG AACTGGCTT CAGTAGTGAA GGCTTCAGTT TTTCGCCAGC TAGGTGTAAA	420
CTGGGACATA GAGTGCTGGA TGAAAGGGGA CTTGACATTA TTCATCTGTC ATATGGAGCC	480
ATTACCTAAG AACCCTTCA AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC	540
TGAAGTCATA GATGATTCGC CTCTGCCCC ACTGAAAGAC AGCTTTCAGA CTGTCCAATG	600
CAACTGCAGT CTTGGGGGAT GTGAATGTCA TGTGCCGGTA CCCAGAGCCA AACTCAACTA	660
CGCTCTTCTG ATGTATTTGG AAATCACATC TGCCGGTGTG AGTTTTCAGT CACCTCTGAT	720
GTCAGTGCAG CCCATGCTTG TTGTGAAACC CGATCCACCC TTAGGTTTGC ATATGGAAGT	780
CACAGATGAT GGTAATTTAA AGATTTCTTG GGACAGCCAA ACAATGGCAC CATTTCCGCT	840
TCAATATCAG GTGAAATATT TAGAGAATTC TACAATTGTA AGAGAGGCTG CTGAAATTGT	900
CTCAGCTACA TCTCTGCTGG TAGACAGTGT GCTTCCTGGA TCTTCATATG AGGTCCAGGT	960
GAGGAGCAAG AGACTGGATG GTTCAGGAGT CTGGAGTGAC TGGAGTTCAC CTCAAGTCTT	1020
TACCACACAA GATGTTGTGT ATTTTCCACC CAAAATTCTG ACTAGTGTTG GATCGAATGC	1080
TTCTTTTCAT TGCATCTACA AAAACGAAAA CCAGATTATC TCCTCAAAAC AGATAGTTTG	1140

GTGGAGGAAT CTAGCTGAGA AAATCCCTGA GATACAGTAC AGCATTGTGA GTGACCGAGT	1200
TAGCAAAGTT ACCTTCTCCA ACCTGAAAGC CACCAGACCT CGAGGGAAGT TTACCTATGA	1260
CGCAGTGTAC TGCTGCAATG AGCAGGCGTG CCATCACCGC TATGCTGAAT TATACGTGAT	1320
CGATGTCAAT ATCAATATAT CATGTGAAAC TGACGGGTAC TTAATAAAA TGACTTGCAG	1380
ATGGTCACCC AGCACAAATCC AATCACTAGT GGAAGCACT GTGCAGCTGA GGTATCACAG	1440
GCGCAGCCTG TATTGTCCTG ATAGTCCATC TATTCATCCT ACGTCTGAGC CCAAAAACTG	1500
CGTCTTACAG AGAGACGGCT TTTATGAATG TGTTCCTCAG CCAATCTTTC TATTATCTGG	1560
CTATACAATG TGGATCAGGA TCAACCATTC TTTAGGTTCA CTTGACTCGC CACCAACGTG	1620
TGTCCTTCCT GACTCCGTAG TAAAACCACT ACCTCCATCT AACGTAAAAG CAGAGATTAC	1680
TGTAAACACT GGATTATTGA AAGTATCTTG GAAAAGCCA GTCTTCCGG AGAATAACCT	1740
TCAATTCCAG ATTCGATATG GCTTAAGTGG AAAAGAAATA CAATGGAAGA CACATGAGGT	1800
ATTCGATGCA AAGTCAAAGT CTGCCAGCCT GCTGCTGTCA GACCTCTGTG CAGTCTATGT	1860
GGTCCAGGTT CGCTGCCGGC GGTGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC	1920
AGCCTATACG CTTGTCATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA	1980
AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTTGGA AGCCCCTGAC	2040
GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCACAA	2100
TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCCTGT GGACAGAACC	2160
AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTTAA	2220
CCTTACCTTC TCATGGCCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC	2280
CCTGAGCAGC AGCTGTGTCA TCCTTTCCTG GACTGTGCA CCTGATGATT ATAGTCTGTT	2340
ATATCTGGTT ATTGAATGGA AGATCCTTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT	2400
TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA	2460
G	2461

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 805 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1				5					10					15	
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys
			20					25					30		
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu
		35					40					45			
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser
	50					55					60				
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro
65					70					75					80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly
				85					90					95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala
			100					105					110		
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp
		115					120					125			
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met
	130					135					140				
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His
145					150					155					160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro
				165					170					175	
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly
			180					185					190		
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu
		195					200					205			
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro
	210					215					220				
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu
225					230					235					240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp
			245						250					255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr
			260					265					270		
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala
		275					280					285			
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
	290					295					300				
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp
305					310					315					320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro  
325 330 335  
Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr  
340 345 350  
Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg  
355 360 365  
Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp  
370 375 380  
Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg  
385 390 395 400  
Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys  
405 410 415  
His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile  
420 425 430  
Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser  
435 440 445  
Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr  
450 455 460  
His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr  
465 470 475 480  
Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys  
485 490 495  
Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg  
500 505 510  
Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu  
515 520 525  
Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu  
530 535 540  
Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val  
545 550 555 560  
Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly  
565 570 575  
Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys  
580 585 590  
Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln  
595 600 605  
Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser  
610 615 620  
Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly  
625 630 635 640  
Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg  
645 650 655  
Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys

660								665				670			
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr
						675	680		685						
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr
						690	695		700						
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala
						705	710		715						
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val
						725	730		735						
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val
						740	745		750						
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu
						755	760		765						
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu
						770	775		780						
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Gly	Met	Cys	Thr
						785	790		795						
						800									
Val Leu Phe Met Asp															
805															

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) FRAGMENT TYPE: C-terminal  
 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala	1	5	10	15
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser	20	25	30	
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val	35	40	45	
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser	50	55	60	
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly	65	70	75	80
Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	Ser	85	90	95	
Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	Asp	100	105	110	
Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	Ser	115	120	125	
Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	Thr	130	135	140	
Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	Ile	145	150	155	160
Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu	Glu	165	170	175	
Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr	Leu	180	185	190	
Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	Gly	195	200	205	
Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser	Asp	210	215	220	
Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	Leu	225	230	235	240
Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln	Phe	245	250	255	

Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys  
260 265 270

Asp Phe Thr Val  
275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Phe Gln Lys Asp Ile Ser His Glu Val Phe Ile Phe Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Ile His Gly Met Cys Thr Val Leu Phe Met Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTGA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr  
1 5 10 15

Ser Glu Pro Lys  
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn  
1 5 10 15

Cys Ser Trp

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTTCCAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA CATGTGGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCCT	120
CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCGATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTCAGGCTC TGTGTTTCATT TGATGTTTCAG	60
AAGTCAGCAA GGTTCATCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA AACTACTTGT GTGTTTTACT	180
TAAAGATACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTTC TCATCTAACA AGCAAGCAAA GGAAGTCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC	60
CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG	180
NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCACTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTGG GTGGTCCACA AAACAACCTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCACT CTATCACATA AAGAAATTCC CAGTGTAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTGCAG	240
AACGATTCCT	250

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC	18
---------------------	----

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG	22
--------------------------	----

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCCTG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 894 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu  
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys  
 20 25 30  
 Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu  
 35 40 45  
 Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser  
 50 55 60  
 Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro  
 65 70 75 80  
 Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly  
 85 90 95  
 Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala  
 100 105 110  
 Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp  
 115 120 125  
 Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met  
 130 135 140  
 Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His  
 145 150 155 160  
 Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro  
 165 170 175  
 Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly  
 180 185 190  
 Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu  
 195 200 205  
 Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro  
 210 215 220  
 Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu  
 225 230 235 240  
 Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp  
 245 250 255  
 Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr  
 260 265 270  
 Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala  
 275 280 285  
 Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val  
 290 295 300  
 Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp  
 305 310 315 320  
 Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro  
 325 330 335  
 Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr  
 340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg  
 355 360 365  
 Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp  
 370 375 380  
 Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg  
 385 390 395 400  
 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys  
 405 410 415  
 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile  
 420 425 430  
 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser  
 435 440 445  
 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr  
 450 455 460  
 His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr  
 465 470 475 480  
 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys  
 485 490 495  
 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg  
 500 505 510  
 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu  
 515 520 525  
 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu  
 530 535 540  
 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val  
 545 550 555 560  
 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly  
 565 570 575  
 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys  
 580 585 590  
 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln  
 595 600 605  
 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser  
 610 615 620  
 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly  
 625 630 635 640  
 Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg  
 645 650 655  
 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys  
 660 665 670  
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr  
 675 680 685  
 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr

690					695					700					
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala
705					710					715					720
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val
			725						730					735	
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val
			740					745						750	
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu
			755				760							765	
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu
			770				775							780	
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile
785					790					795					800
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly
			805						810					815	
Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp
			820					825						830	
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile
			835				840							845	
Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg
			850				855							860	
Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser
865					870					875					880
Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Arg	Thr	Asp	Thr	Leu		
				885					890						

"(2) INFORMATION FOR SEQ ID NO:56:

" (i) SEQUENCE CHARACTERISTICS:  
 " (A) LENGTH: 1165 amino acids  
 " (B) TYPE: amino acid  
 " (C) STRANDEDNESS: single  
 " (D) TOPOLOGY: linear  
 "

" (ii) MOLECULE TYPE: protein  
 "

" (iii) HYPOTHETICAL: NO  
 "

" (vi) ORIGINAL SOURCE:  
 " (A) ORGANISM: Homo sapiens  
 "

" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
 "

Met	Ile	Cys	Gln	Lys	Phe	Cys	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Ile
1				5					10					15	
Tyr	Val	Ile	Thr	Ala	Phe	Asn	Leu	Ser	Tyr	Pro	Ile	Thr	Pro	Trp	Arg
			20					25					30		

" Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu  
 " 35 40 45  
 " Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr  
 " 50 55 60  
 " Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser  
 " 65 70 75 80  
 " Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp  
 " 85 90 95  
 " Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val  
 " 100 105 110  
 " Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn  
 " 115 120 125  
 " Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val  
 " 130 135 140  
 " Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His  
 " 145 150 155 160  
 " Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro  
 " 165 170 175  
 " Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu  
 " 180 185 190  
 " Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr  
 " 195 200 205  
 " Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser  
 " 210 215 220  
 " Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro  
 " 225 230 235 240  
 " Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser  
 " 245 250 255  
 " Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys  
 " 260 265 270  
 " Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val  
 " 275 280 285  
 " Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr  
 " 290 295 300  
 " Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser  
 " 305 310 315 320  
 " Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe  
 " 325 330 335  
 " Pro Pro Lys Ile Leu Thr Ser Val Gly Ser Asn Val Ser Phe His Cys  
 " 340 345 350  
 " Ile Tyr Lys Lys Glu Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp  
 " 355 360 365  
 " Trp Met Asn Leu Ala Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val

370	375	380
Ser 385	Asp 390	His 395
Val 400	Ser 405	Thr 410
Pro 415	Arg 420	Gly 425
Lys 430	Phe 435	Thr 440
Glu 445	Cys 450	His 455
Asn 460	Ile 465	Val 470
Thr 475	Cys 480	Arg 485
Trp 490	Ser 495	Thr 500
Leu 505	Gln 510	Thr 515
Arg 520	Tyr 525	His 530
Pro 535	Ile 540	Ser 545
Glu 550	Cys 555	Thr 560
Met 565	Trp 570	Thr 575
Ile 580	Arg 585	Thr 590
Val 595	Pro 600	Thr 605
Ala 610	Glu 615	Thr 620
Pro 625	Val 630	Thr 635
Ser 640	Thr 645	Thr 650
Arg 655	Gly 660	Thr 665
Glu 670	Lys 675	Thr 680
Asn 685	Thr 690	Thr 695
Thr 700	Thr 705	Thr 710
Thr 715	Thr 720	Thr 725

Gly Ala Ser Val Ala Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser  
 725 730 735  
 Lys Val Asn Ile Val Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser  
 740 745 750  
 Cys Val Ile Val Ser Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met  
 755 760 765  
 Tyr Phe Ile Ile Glu Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys  
 770 775 780  
 Trp Leu Arg Ile Ser Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His  
 785 790 795 800  
 Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met  
 805 810 815  
 Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp  
 820 825 830  
 Ile Glu Lys His Gln Ser Asp Ala Gly Leu Tyr Val Ile Val Pro Val  
 835 840 845  
 Ile Ile Ser Ser Ser Ile Leu Leu Leu Gly Thr Leu Leu Ile Ser His  
 850 855 860  
 Gln Arg Met Lys Lys Leu Phe Trp Glu Asp Val Pro Asn Pro Lys Asn  
 865 870 875 880  
 Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu  
 885 890 895  
 His Leu Phe Ile Lys His Thr Ala Ser Val Thr Cys Gly Pro Leu Leu  
 900 905 910  
 Leu Glu Pro Glu Thr Ile Ser Glu Asp Ile Ser Val Asp Thr Ser Trp  
 915 920 925  
 Lys Asn Lys Asp Glu Met Met Pro Thr Thr Val Val Ser Leu Leu Ser  
 930 935 940  
 Thr Thr Asp Leu Glu Lys Gly Ser Val Cys Ile Ser Asp Gln Phe Asn  
 945 950 955 960  
 Ser Val Asn Phe Ser Glu Ala Glu Gly Thr Glu Val Thr Tyr Glu Ala  
 965 970 975  
 Glu Ser Gln Arg Gln Pro Phe Val Lys Tyr Ala Thr Leu Ile Ser Asn  
 980 985 990  
 Ser Lys Pro Ser Glu Thr Gly Glu Glu Gln Gly Leu Ile Asn Ser Ser  
 995 1000 1005  
 Val Thr Lys Cys Phe Ser Ser Lys Asn Ser Pro Leu Lys Asp Ser Phe  
 1010 1015 1020  
 Ser Asn Ser Ser Trp Glu Ile Glu Ala Gln Ala Phe Phe Ile Leu Ser  
 1025 1030 1035 1040  
 Asp Gln His Pro Asn Ile Ile Ser Pro His Leu Thr Phe Ser Glu Gly  
 1045 1050 1055

Leu Asp Glu Leu Leu Lys Leu Glu Gly Asn Phe Pro Glu Glu Asn Asn  
1060 1065 1070

Asp Lys Lys Ser Ile Tyr Tyr Leu Gly Val Thr Ser Ile Lys Lys Arg  
1075 1080 1085

Glu Ser Gly Val Leu Leu Thr Asp Lys Ser Arg Val Ser Cys Pro Phe  
1090 1095 1100

Pro Ala Pro Cys Leu Phe Thr Asp Ile Arg Val Leu Gln Asp Ser Cys  
1105 1110 1115 1120

Ser His Phe Val Glu Asn Asn Ile Asn Leu Gly Thr Ser Ser Lys Lys  
1125 1130 1135

Thr Phe Ala Ser Tyr Met Pro Gln Phe Gln Thr Cys Ser Thr Gln Thr  
1140 1145 1150

His Lys Ile Met Glu Asn Lys Met Cys Asp Leu Thr Val  
1155 1160 1165

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B1  
cont